

SEQUENCE LISTING

<110> ZENSUN(SHANGHAI)SCIENCE AND TECHNOLOGY LIMITED

<120> ERBB3 BASED METHODS AND COMPOSITIONS FOR TREATING NEOPLASMS

<130> 52401-20003.00

<160> 16

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1342

<212> PRT

<213> Homo sapiens

<400> 1

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      20             25             30
Leu Asn Gly Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr
      35             40             45
Leu Tyr Lys Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu
      50             55             60
Ile Val Leu Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile
      65             70             75             80
Arg Glu Val Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr
      85             90             95
Leu Pro Leu Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp
      100            105            110
Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser
      115            120            125
His Ala Leu Arg Gln Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser
      130            135            140
Gly Gly Val Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr

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145 150 155 160
 Ile Asp Trp Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val
 165 170 175
 Lys Asp Asn Gly Arg Ser Cys Pro Pro Cys His Glu Val Cys Lys Gly
 180 185 190
 Arg Cys Trp Gly Pro Gly Ser Glu Asp Cys Gln Thr Leu Thr Lys Thr
 195 200 205
 Ile Cys Ala Pro Gln Cys Asn Gly His Cys Phe Gly Pro Asn Pro Asn
 210 215 220
 Gln Cys Cys His Asp Glu Cys Ala Gly Gly Cys Ser Gly Pro Gln Asp
 225 230 235 240
 Thr Asp Cys Phe Ala Cys Arg His Phe Asn Asp Ser Gly Ala Cys Val
 245 250 255
 Pro Arg Cys Pro Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe Gln Leu
 260 265 270
 Glu Pro Asn Pro His Thr Lys Tyr Gln Tyr Gly Gly Val Cys Val Ala
 275 280 285
 Ser Cys Pro His Asn Phe Val Val Asp Gln Thr Ser Cys Val Arg Ala
 290 295 300
 Cys Pro Pro Asp Lys Met Glu Val Asp Lys Asn Gly Leu Lys Met Cys
 305 310 315 320
 Glu Pro Cys Gly Gly Leu Cys Pro Lys Ala Cys Glu Gly Thr Gly Ser
 325 330 335
 Gly Ser Arg Phe Gln Thr Val Asp Ser Ser Asn Ile Asp Gly Phe Val
 340 345 350
 Asn Cys Thr Lys Ile Leu Gly Asn Leu Asp Phe Leu Ile Thr Gly Leu
 355 360 365
 Asn Gly Asp Pro Trp His Lys Ile Pro Ala Leu Asp Pro Glu Lys Leu
 370 375 380
 Asn Val Phe Arg Thr Val Arg Glu Ile Thr Gly Tyr Leu Asn Ile Gln
 385 390 395 400
 Ser Trp Pro Pro His Met His Asn Phe Ser Val Phe Ser Asn Leu Thr
 405 410 415
 Thr Ile Gly Gly Arg Ser Leu Tyr Asn Arg Gly Phe Ser Leu Leu Ile
 420 425 430
 Met Lys Asn Leu Asn Val Thr Ser Leu Gly Phe Arg Ser Leu Lys Glu
 435 440 445

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Ile Ser Ala Gly Arg Ile Tyr Ile Ser Ala Asn Arg Gln Leu Cys Tyr
  450                      455                      460
His His Ser Leu Asn Trp Thr Lys Val Leu Arg Gly Pro Thr Glu Glu
  465                      470                      475                      480
Arg Leu Asp Ile Lys His Asn Arg Pro Arg Arg Asp Cys Val Ala Glu
                      485                      490                      495
Gly Lys Val Cys Asp Pro Leu Cys Ser Ser Gly Gly Cys Trp Gly Pro
                      500                      505                      510
Gly Pro Gly Gln Cys Leu Ser Cys Arg Asn Tyr Ser Arg Gly Gly Val
                      515                      520                      525
Cys Val Thr His Cys Asn Phe Leu Asn Gly Glu Pro Arg Glu Phe Ala
                      530                      535                      540
His Glu Ala Glu Cys Phe Ser Cys His Pro Glu Cys Gln Pro Met Glu
  545                      550                      555                      560
Gly Thr Ala Thr Cys Asn Gly Ser Gly Ser Asp Thr Cys Ala Gln Cys
                      565                      570                      575
Ala His Phe Arg Asp Gly Pro His Cys Val Ser Ser Cys Pro His Gly
                      580                      585                      590
Val Leu Gly Ala Lys Gly Pro Ile Tyr Lys Tyr Pro Asp Val Gln Asn
                      595                      600                      605
Glu Cys Arg Pro Cys His Glu Asn Cys Thr Gln Gly Cys Lys Gly Pro
                      610                      615                      620
Glu Leu Gln Asp Cys Leu Gly Gln Thr Leu Val Leu Ile Gly Lys Thr
  625                      630                      635                      640
His Leu Thr Met Ala Leu Thr Val Ile Ala Gly Leu Val Val Ile Phe
                      645                      650                      655
Met Met Leu Gly Gly Thr Phe Leu Tyr Trp Arg Gly Arg Arg Ile Gln
                      660                      665                      670
Asn Lys Arg Ala Met Arg Arg Tyr Leu Glu Arg Gly Glu Ser Ile Glu
                      675                      680                      685
Pro Leu Asp Pro Ser Glu Lys Ala Asn Lys Val Leu Ala Arg Ile Phe
  690                      695                      700
Lys Glu Thr Glu Leu Arg Lys Leu Lys Val Leu Gly Ser Gly Val Phe
  705                      710                      715                      720
Gly Thr Val His Lys Gly Val Trp Ile Pro Glu Gly Glu Ser Ile Lys
                      725                      730                      735
Ile Pro Val Cys Ile Lys Val Ile Glu Asp Lys Ser Gly Arg Gln Ser

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	740		745		750										
Phe	Gln	Ala	Val	Thr	Asp	His	Met	Leu	Ala	Ile	Gly	Ser	Leu	Asp	His
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Ala	His	Ile	Val	Arg	Leu	Leu	Gly	Leu	Cys	Pro	Gly	Ser	Ser	Leu	Gln
	770						775					780			
Leu	Val	Thr	Gln	Tyr	Leu	Pro	Leu	Gly	Ser	Leu	Leu	Asp	His	Val	Arg
785					790					795					800
Gln	His	Arg	Gly	Ala	Leu	Gly	Pro	Gln	Leu	Leu	Leu	Asn	Trp	Gly	Val
			805					810						815	
Gln	Ile	Ala	Lys	Gly	Met	Tyr	Tyr	Leu	Glu	Glu	His	Gly	Met	Val	His
		820						825					830		
Arg	Asn	Leu	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
		835						840					845		
Gln	Val	Ala	Asp	Phe	Gly	Val	Ala	Asp	Leu	Leu	Pro	Pro	Asp	Asp	Lys
	850					855					860				
Gln	Leu	Leu	Tyr	Ser	Glu	Ala	Lys	Thr	Pro	Ile	Lys	Trp	Met	Ala	Leu
865					870					875				880	
Glu	Ser	Ile	His	Phe	Gly	Lys	Tyr	Thr	His	Gln	Ser	Asp	Val	Trp	Ser
			885					890						895	
Tyr	Gly	Val	Thr	Val	Trp	Glu	Leu	Met	Thr	Phe	Gly	Ala	Glu	Pro	Tyr
		900						905					910		
Ala	Gly	Leu	Arg	Leu	Ala	Glu	Val	Pro	Asp	Leu	Leu	Glu	Lys	Gly	Glu
	915						920						925		
Arg	Leu	Ala	Gln	Pro	Gln	Ile	Cys	Thr	Ile	Asp	Val	Tyr	Met	Val	Met
	930					935							940		
Val	Lys	Cys	Trp	Met	Ile	Asp	Glu	Asn	Ile	Arg	Pro	Thr	Phe	Lys	Glu
945					950					955				960	
Leu	Ala	Asn	Glu	Phe	Thr	Arg	Met	Ala	Arg	Asp	Pro	Pro	Arg	Tyr	Leu
			965						970					975	
Val	Ile	Lys	Arg	Glu	Ser	Gly	Pro	Gly	Ile	Ala	Pro	Gly	Pro	Glu	Pro
		980						985					990		
His	Gly	Leu	Thr	Asn	Lys	Lys	Leu	Glu	Glu	Val	Glu	Leu	Glu	Pro	Glu
	995						1000						1005		
Leu	Asp	Leu	Asp	Leu	Asp	Leu	Glu	Ala	Glu	Glu	Asp	Asn	Leu	Ala	Thr
	1010					1015						1020			
Thr	Thr	Leu	Gly	Ser	Ala	Leu	Ser	Leu	Pro	Val	Gly	Thr	Leu	Asn	Arg
1025					1030					1035				1040	

Pro Arg Gly Ser Gln Ser Leu Leu Ser Pro Ser Ser Gly Tyr Met Pro
 1045 1050 1055
 Met Asn Gln Gly Asn Leu Gly Glu Ser Cys Gln Glu Ser Ala Val Ser
 1060 1065 1070
 Gly Ser Ser Glu Arg Cys Pro Arg Pro Val Ser Leu His Pro Met Pro
 1075 1080 1085
 Arg Gly Cys Leu Ala Ser Glu Ser Ser Glu Gly His Val Thr Gly Ser
 1090 1095 1100
 Glu Ala Glu Leu Gln Glu Lys Val Ser Met Cys Arg Ser Arg Ser Arg
 1105 1110 1115 1120
 Ser Arg Ser Pro Arg Pro Arg Gly Asp Ser Ala Tyr His Ser Gln Arg
 1125 1130 1135
 His Ser Leu Leu Thr Pro Val Thr Pro Leu Ser Pro Pro Gly Leu Glu
 1140 1145 1150
 Glu Glu Asp Val Asn Gly Tyr Val Met Pro Asp Thr His Leu Lys Gly
 1155 1160 1165
 Thr Pro Ser Ser Arg Glu Gly Thr Leu Ser Ser Val Gly Leu Ser Ser
 1170 1175 1180
 Val Leu Gly Thr Glu Glu Glu Asp Glu Asp Glu Glu Tyr Glu Tyr Met
 1185 1190 1195 1200
 Asn Arg Arg Arg Arg His Ser Pro Pro His Pro Pro Arg Pro Ser Ser
 1205 1210 1215
 Leu Glu Glu Leu Gly Tyr Glu Tyr Met Asp Val Gly Ser Asp Leu Ser
 1220 1225 1230
 Ala Ser Leu Gly Ser Thr Gln Ser Cys Pro Leu His Pro Val Pro Ile
 1235 1240 1245
 Met Pro Thr Ala Gly Thr Thr Pro Asp Glu Asp Tyr Glu Tyr Met Asn
 1250 1255 1260
 Arg Gln Arg Asp Gly Gly Gly Pro Gly Gly Asp Tyr Ala Ala Met Gly
 1265 1270 1275 1280
 Ala Cys Pro Ala Ser Glu Gln Gly Tyr Glu Glu Met Arg Ala Phe Gln
 1285 1290 1295
 Gly Pro Gly His Gln Ala Pro His Val His Tyr Ala Arg Leu Lys Thr
 1300 1305 1310
 Leu Arg Ser Leu Glu Ala Thr Asp Ser Ala Phe Asp Asn Pro Asp Tyr
 1315 1320 1325
 Trp His Ser Arg Leu Phe Pro Lys Ala Asn Ala Gln Arg Thr

1330

1335

1340

<210> 2

<211> 640

<212> PRT

<213> Homo sapiens

<400> 2

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Met Arg Ala Asn Asp Ala Leu Gln Val Leu Gly Leu Leu Phe Ser Leu
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Ala Arg Gly Ser Glu Val Gly Asn Ser Gln Ala Val Cys Pro Gly Thr
      20           25           30
Leu Asn Gly Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr
      35           40           45
Leu Tyr Lys Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu
      50           55           60
Ile Val Leu Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile
      65           70           75           80
Arg Glu Val Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr
      85           90           95
Leu Pro Leu Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp
      100           105           110
Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser
      115           120           125
His Ala Leu Arg Gln Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser
      130           135           140
Gly Gly Val Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr
      145           150           155           160
Ile Asp Trp Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val
      165           170           175
Lys Asp Asn Gly Arg Ser Cys Pro Pro Cys His Glu Val Cys Lys Gly
      180           185           190
Arg Cys Trp Gly Pro Gly Ser Glu Asp Cys Gln Thr Leu Thr Lys Thr
      195           200           205
Ile Cys Ala Pro Gln Cys Asn Gly His Cys Phe Gly Pro Asn Pro Asn
      210           215           220
Gln Cys Cys His Asp Glu Cys Ala Gly Gly Cys Ser Gly Pro Gln Asp

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225          230          235          240
Thr Asp Cys Phe Ala Cys Arg His Phe Asn Asp Ser Gly Ala Cys Val
          245          250          255
Pro Arg Cys Pro Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe Gln Leu
          260          265          270
Glu Pro Asn Pro His Thr Lys Tyr Gln Tyr Gly Gly Val Cys Val Ala
          275          280          285
Ser Cys Pro His Asn Phe Val Val Asp Gln Thr Ser Cys Val Arg Ala
          290          295          300
Cys Pro Pro Asp Lys Met Glu Val Asp Lys Asn Gly Leu Lys Met Cys
          305          310          315          320
Glu Pro Cys Gly Gly Leu Cys Pro Lys Ala Cys Glu Gly Thr Gly Ser
          325          330          335
Gly Ser Arg Phe Gln Thr Val Asp Ser Ser Asn Ile Asp Gly Phe Val
          340          345          350
Asn Cys Thr Lys Ile Leu Gly Asn Leu Asp Phe Leu Ile Thr Gly Leu
          355          360          365
Asn Gly Asp Pro Trp His Lys Ile Pro Ala Leu Asp Pro Glu Lys Leu
          370          375          380
Asn Val Phe Arg Thr Val Arg Glu Ile Thr Gly Tyr Leu Asn Ile Gln
          385          390          395          400
Ser Trp Pro Pro His Met His Asn Phe Ser Val Phe Ser Asn Leu Thr
          405          410          415
Thr Ile Gly Gly Arg Ser Leu Tyr Asn Arg Gly Phe Ser Leu Leu Ile
          420          425          430
Met Lys Asn Leu Asn Val Thr Ser Leu Gly Phe Arg Ser Leu Lys Glu
          435          440          445
Ile Ser Ala Gly Arg Ile Tyr Ile Ser Ala Asn Arg Gln Leu Cys Tyr
          450          455          460
His His Ser Leu Asn Trp Thr Lys Val Leu Arg Gly Pro Thr Glu Glu
          465          470          475          480
Arg Leu Asp Ile Lys His Asn Arg Pro Arg Arg Asp Cys Val Ala Glu
          485          490          495
Gly Lys Val Cys Asp Pro Leu Cys Ser Ser Gly Gly Cys Trp Gly Pro
          500          505          510
Gly Pro Gly Gln Cys Leu Ser Cys Arg Asn Tyr Ser Arg Gly Gly Val
          515          520          525

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Cys Val Thr His Cys Asn Phe Leu Asn Gly Glu Pro Arg Glu Phe Ala
 530 535 540
 His Glu Ala Glu Cys Phe Ser Cys His Pro Glu Cys Gln Pro Met Glu
 545 550 555 560
 Gly Thr Ala Thr Cys Asn Gly Ser Gly Ser Asp Thr Cys Ala Gln Cys
 565 570 575
 Ala His Phe Arg Asp Gly Pro His Cys Val Ser Ser Cys Pro His Gly
 580 585 590
 Val Leu Gly Ala Lys Gly Pro Ile Tyr Lys Tyr Pro Asp Val Gln Asn
 595 600 605
 Glu Cys Arg Pro Cys His Glu Asn Cys Thr Gln Gly Cys Lys Gly Pro
 610 615 620
 Glu Leu Gln Asp Cys Leu Gly Gln Thr Leu Val Leu Ile Gly Lys Thr
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<210> 3

<211> 190

<212> PRT

<213> Homo sapiens

<400> 3

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 20 25 30
 Leu Asn Gly Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr
 35 40 45
 Leu Tyr Lys Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu
 50 55 60
 Ile Val Leu Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile
 65 70 75 80
 Arg Glu Val Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr
 85 90 95
 Leu Pro Leu Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp
 100 105 110
 Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser
 115 120 125

His Ala Leu Arg Gln Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser
 130 135 140
 Gly Gly Val Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr
 145 150 155 160
 Ile Asp Trp Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val
 165 170 175
 Lys Asp Asn Gly Arg Ser Cys Pro Pro Cys His Glu Val Cys
 180 185 190

<210> 4

<211> 1914

<212> DNA

<213> Homo sapiens

<400> 4

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gtgggcaact ctcaggcagt gtgtcctggg actctgaatg gcctgagtgt gaccggcgat      120
gctgagaacc aataccagac actgtacaag ctctacgaga ggtgtgaggt ggtgatgggg      180
aaccttgaga ttgtgctcac gggacacaat gccgacctct ccttcctgca gtggattcga      240
gaagtgacag gctatgtcct cgtggccatg aatgaattct ctactctacc attgcccac      300
ctcccgctgg tgcgagggac ccaggtctac gatgggaagt ttgccatctt cgtcatgttg      360
aactataaca ccaactccag ccacgctctg cgccagctcc gcttgactca gctcaccgag      420
attctgtcag ggggtgttta tattgagaag aacgataagc tttgtcacat ggacacaatt      480
gactggaggg acatcgtgag ggaccgagat gctgagatag tgggtgaagga caatggcaga      540
agctgtcccc cctgtcatga ggtttgcaag gggcgatgct ggggtcctgg atcagaagac      600
tgccagacat tgaccaagac catctgtgct cctcagtgtg atggtcactg ctttggggcc      660
aaccccaacc agtgctgcca tgatgagtgt gccgggggct gctcaggccc tcaggacaca      720
gactgctttg cctgccggca cttcaatgac agtggagcct gtgtacctcg ctgtccacag      780
cctcttgtct acaacaagct aactttccag ctggaacca atccccacac caagtatcag      840
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gtcagggcct gtcctcctga caagatggaa gtagataaaa atgggctcaa gatgtgtgag      960
ccttgtaggg gactatgtcc caaagcctgt gagggaacag gctctgggag ccgcttcag     1020
actgtggact cgagcaacat tgatggattt gtgaactgca ccaagatcct gggcaacctg     1080
gactttctga tcaccggcct caatggagac ccctggcaca agatccctgc cctggaccca     1140
gagaagctca atgtcttccg gacagtacgg gagatcacag gttacctgaa catccagtcc     1200
tgggcgcccc acatgcacaa cttcagtgtt ttttccaatt tgacaacat tggaggcaga     1260
agcctctaca accggggcct ctcattgttg atcatgaaga acttgaatgt cacatctctg     1320

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ggcttccgat ccctgaagga aattagtgtt gggcgatatc atataagtgc caataggcag 1380
ctctgtctacc accactcttt gaactggacc aagggtgttc gggggcctac ggaagagcga 1440
ctagacatca agcataatcg gccgcgcaga gactgcgtgg cagagggcaa agtgtgtgac 1500
ccactgtgtc cctctggggg atgtctgggg ccaggccctg gtcagtgtt gtctgtctga 1560
aattatagcc gaggaggtgt ctgtgtgacc cactgcaact ttctgaatgg ggagcctcga 1620
gaatttgccc atgaggccga atgcttctcc tgccaccgga aatgccaaac catggagggc 1680
actgccacat gcaatggctc gggctctgat acttgtgtc aatgtgcca tttctgagat 1740
ggggcccaact gtgtgagcag ctgcccccat ggagtcctag gtgccaaggg cccaatctac 1800
aagtaccacg atgttcagaa tgaatgtcgg ccctgccatg agaactgcac ccaggggtgt 1860
aaaggaccag agcttcaaga ctgttttaga caaacactgg tgctgatcgg caaa 1914

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<210> 5

<211> 475

<212> DNA

<213> Homo sapiens

<400> 5

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tcacgggaca caatgccgac ctctccttcc tgcagtggat tcgagaagtg acaggctatg 180
tcctcgtggc catgaatgaa ttctctactc taccattgcc caacctccgc gtggtgagag 240
ggacccaggc ctacgatggg aagtttgcca tcttcgtcat gttgaactat aacaccaact 300
ccagccacgc tctgcgccag ctccgcttga ctgagctcac cgagattctg tcaggggggtg 360
tttatattga gaagaacgat aagctttgtc acatggacac aattgactgg agggacatcg 420
tgagggaccg agatgctgag atagtgtgga aggacaatgg cagaagctga ctcca 475

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<210> 6

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 6

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<210> 7
<211> 48
<212> DNA
<213> Artificial Sequence

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<400> 7
tgtgaccacg actagccgtt tctgatgttc ctgctactgc tgttcact 48

<210> 8
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 8
tctagagatt ttctgcggag tcatg 25

<210> 9
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 9
gacgacgacg acaag 15

<210> 10
<211> 16
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer

<400> 10

gccatggctg atatcg

16

<210> 11

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 11

gcaccaccac caccaccact gag

23

<210> 12

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 12

acatcaagca taatcggcc

19

<210> 13

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 13

aggctcccca ttcagaaag

19

<210> 14

<211> 82

<212> PRT

<213> Homo sapiens

<400> 14

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Gly	Pro	Thr	Glu	Glu	Arg	Leu	Asp	Ile	Lys	His	Asn	Arg	Pro	Arg	Arg
			20					25					30		
Asp	Cys	Val	Ala	Glu	Gly	Lys	Val	Cys	Asp	Pro	Leu	Cys	Ser	Ser	Gly
		35					40					45			
Gly	Cys	Trp	Gly	Pro	Gly	Pro	Gly	Gln	Cys	Leu	Ser	Cys	Arg	Asn	Tyr
	50					55				60					
Ser	Arg	Gly	Gly	Val	Cys	Val	Thr	His	Cys	Asn	Phe	Leu	Asn	Gly	Glu
65				70						75				80	
Pro	Arg														

<210> 15

<211> 456

<212> DNA

<213> Homo sapiens

<400> 15

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gggggactat	gtcccaaagc	ctgtgagggg	acaggctctg	ggagccgctt	ccagactgtg	180
gactcgagca	acattgatgg	atttgtgaac	tgcaccaaga	tcctgggcaa	cctggacttt	240
ctgatcaccg	gcctcaatgg	agaccctgg	cacaagatcc	ctgccctgga	cccagagaag	300
ctcaatgtct	tccggacagt	acgggagatc	acaggttacc	tgaacatcca	gtcctggccg	360
ccccacatgc	acaacttcag	tgttttttcc	aatttgacaa	ccattggagg	cagaaagctt	420
gcggccgcac	tcgagcacca	ccaccaccac	cactga			456

<210> 16

<211> 148

<212> PRT

<213> Homo sapiens

<400> 16

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Ser Cys Val Arg Ala Cys Pro Pro Asp Lys Met Glu Val Asp Lys Asn
          20           25           30
Gly Leu Lys Met Cys Glu Pro Cys Gly Gly Leu Cys Pro Lys Ala Cys
          35           40           45
Glu Gly Thr Gly Ser Gly Ser Arg Phe Gln Thr Val Asp Ser Ser Asn
          50           55           60
Ile Asp Gly Phe Val Asn Cys Thr Lys Ile Leu Gly Asn Leu Asp Phe
65           70           75           80
Leu Ile Thr Gly Leu Asn Gly Asp Pro Trp His Lys Ile Pro Ala Leu
          85           90           95
Asp Pro Glu Lys Leu Asn Val Phe Arg Thr Val Arg Glu Ile Thr Gly
          100          105          110
Tyr Leu Asn Ile Gln Ser Trp Pro Pro His Met His Asn Phe Ser Val
          115          120          125
Phe Ser Asn Leu Thr Thr Ile Gly Gly Arg Ser Leu Tyr Asn Arg Gly
          130          135          140
Phe Ser Leu Leu
145

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